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SEQUENCE LISTING

<110> Burkly, Linda C.

<120> TREATMENT FOR INSULIN DEPENDENT DIABETES

<130> 10274-008003

<140> US 09/234,290

<141> 1999-01-20

<150> US 08/447,118

<151> 1995-05-22

<150> US 08/029,330

<151> 1993-02-09

<150> PCT/US94/01456

<151> 1994-02-09

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> pBAG159 insert: HP1/2 heavy chain variable region;
amino acid 1 is Glu (E) but Gln (Q) may be
substituted

<221> CDS

<222> (1)...(360)

<400> 1

gtc aaa ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc tca
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

48

gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc tat
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30

96

atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att gga
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
35 40 45

144

agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc cag
Arg Ile Asp Pro Ala Ser Gly Asp Thr Tyr Asp Pro Lys Phe Gln

192

50	55	60	
gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg ctg			240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu			
65	70	75	80
cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt gca			288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala			
85	90	95	
gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc caa			336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln			
100	105	110	
ggg acc acg gtc acc gtc tcc tca			360
Gly Thr Thr Val Thr Val Ser Ser			
115	120		

<210> 2
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 2
 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1 5 10 15
 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
 20 25 30
 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
 35 40 45
 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
 50 55 60
 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65 70 75 80
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 3
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> pBAG172 insert: HP1/2 light chain variable region

 <221> CDS
 <222> (1)...(318)
 <223> HP1/2 light chain variable region

 <400> 3

agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga	48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly	
1 5 10 15	
gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat	96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp	
20 25 30	
gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata	144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
35 40 45	
tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc	192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
50 55 60	
agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct	240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala	
65 70 75 80	
gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac	288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr	
85 90 95	
acg ttc gga ggg acc aag ctg gag atc	318
Thr Phe Gly Gly Thr Lys Leu Glu Ile	
100 105	

E/w

<210> 4
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 4
 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gly Thr Lys Leu Glu Ile
 100 105

<210> 5
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1) ... (429)

<221> sig_peptide
<222> (1) ... (57)

<221> mat_peptide
<222> (58) ... (429)

<221> misc_feature
<222> (0) ... (0)
<223> pBAG195 insert: AS heavy chain variable region

<400> 5
atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gca cca ggt 48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-15 -10 -5

gcc cac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
1 5 10

cct agc cag acc ctg agc ctg acc tgc acc gcg tct ggc ttc aac att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
15 20 25

aaa gac acc tat atg cac tgg gtg aga cag cca cct gga cga ggt ctt 192
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30 35 40 45

gag tgg att gga agg att gat cct gcg agt ggc gat act aaa tat gac 240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

ccg aag ttc cag gtc aga gtg aca atg ctg gta gac acc agc agc aac 288
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
65 70 75

cag ttc agc ctg aga ctc agc agc gtg aca gcc gac acc gac acc gtc 336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
80 85 90

tat tat tgt gca gac gga atg tgg gta tca acg gga tat gct ctg gac 384
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
95 100 105

ttc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gag tcc 429
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110 115 120

<210> 6
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> (1) . . . (19)

<400> 6

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Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
          -15           -10           -5
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
          1             5             10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
          15            20            25
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
          30            35            40            45
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
          50            55            60
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
          65            70            75
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
          80            85            90
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
          95           100           105
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
          110          115          120

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<210> 7

<211> 386

<212> DNA

<213> *Homo sapiens*

<220>

<221> CDS

<222> (1) . . . (384)

<221> sig_peptide
<222> (1) ... (57)

<221> mat_peptide
<222> (58) ... (384)

<221> misc_feature

<222> (0) . . . (0)

<223> pBAG198 insert: VK2 (SVMDY) light chain variable region

<400> 7

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atg ggt tgg tcc tgc atc atc ctg ttc ctg gtt gct acc gct acc acc ggt
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-15           -10           -5

```

48

gtc cac tcc agc atc gtg atg acc cag agc cca agc agc ctg agc gcc
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

96

agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag agt gtg
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
15 20 25

144

act aat gat gta gct tgg tac cag cag aag cca ggt aag gct cca aag
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

192

30	35	40	45	
ctg ctg atc tac tat gca tcc aat cgc tac act ggt gtg cca gat aga				240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg				
50	55	60		
ttc agc ggt agc ggt tat ggt acc gac ttc acc ttc acc atc agc agc				288
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser				
65	70	75		
ctc cag cca gag gac atc gcc acc tac tac tgc cag cag gat tat agc				336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser				
80	85	90		
tct ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt aag				384
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys				
95	100	105		
tg				386
<p><210> 8 <211> 128 <212> PRT <213> Homo sapiens</p>				
<p><220> <221> SIGNAL <222> (1) ... (19)</p>				
<p><i>E1</i> <i>Cut</i></p>				
<p><400> 8 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly -15 -10 -5 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val 15 20 25 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg 50 55 60 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser 80 85 90 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 95 100 105</p>				
<p><210> 9 <211> 1347 <212> DNA <213> Homo sapiens</p>				
<p><220> <221> CDS <222> (1) ... (1338)</p>				
<p><221> misc_feature</p>				

<222> (1)...(219)

<223> VCAM-1 gene segment: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc_feature

<222> (220)...(229)

<223> Hinge region: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc_feature

<222> (230)...(338)

<223> Heavy chain constant region 2: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.

<221> misc_feature

<222> (339)...(446)

<223> Heavy chain constant region 3: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

<400> 9

atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
1 5 10 15

48

ata atg ttt gca gct tct caa gct ttt aaa atc gag acc acc cca gaa
Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
20 25 30

96

tct aga tat ctt gct cag att ggt gac tcc gtc tca ttg act tgc agc
Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
35 40 45

144

acc aca ggc tgt gag tcc cca ttt ttc tct tgg aga acc cag ata gat
Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
50 55 60

192

agt cca ctg aat ggg aag gtc acg aat gag ggg acc aca tct acg ctg
Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Ser Thr Leu
65 70 75 80

240

aca atg aat cct gtt agt ttt ggg aac gaa cac tct tac ctg tgc aca
Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
85 90 95

288

gca act tgt gaa tct agg aaa ttg gaa aaa gga atc cag gtc gag atc
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile

336

100	105	110	
tac tct ttt cct aag gat cca gag att cat ttg agt ggc cct ctg gag Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu 115 120 125			384
gct ggg aag ccg atc aca gtc aag tgt tca gtt gct gat gta tac cca Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro 130 135 140			432
ttt gac agg ctg gag ata gac tta ctg aaa gga gat cat ctc atg aag Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys 145 150 155 160			480
agt cag gaa ttt ctg gag gat gca gac agg aag tcc ctg gaa acc aag Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys 165 170 175			528
agt ttg gaa gta acc ttt act cct gtc att gag gat att gga aaa gtt Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val 180 185 190			576
ctt gtt tgc cga gct aaa tta cac att gat gaa atg gat tct gtg ccc Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro 195 200 205			624
aca gta agg cag gct gta aaa gaa ttg caa gtc gac aaa act cac aca Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr 210 215 220			672
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe 225 230 235 240			720
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cg acc cct Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 245 250 255			768
gag gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val 260 265 270			816
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 275 280 285			864
aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 290 295 300			912
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 305 310 315 320			960
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 325 330 335			1008

E
1
c
y

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca	1056
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
340	345
350	
tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc	1104
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	
355	360
365	
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg	1152
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
370	375
380	
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac	1200
Gln Pro Glu Asn Asn Tyr Thr Pro Pro Val Leu Asp Ser Asp	
385	390
395	400
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg	1248
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
405	410
415	
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac	1296
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
420	425
430	
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa	1338
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
435	440
445	
tgagtgcgg	1347
<i>E1</i>	
<210> 10	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> oligonucleotide for PCR	
<400> 10	
tcgtcgacaa aactcacaca tgcc	24
<210> 11	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> oligonucleotide for PCR	
<400> 11	
gttaaatagt gcggcgccg ccaa	24
<210> 12	
<211> 115	

<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

<400> 12
gcggccgcgg tccaaaccacc aatctcaaag cttggtaccc gggattcag atctgcagca
tgctcgagct ctagatatcg attccatgga tcctcacatc ccaatccgcg gcccgc

60
115

<210> 13
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

<400> 13
gagctcgagg cggccgcacc atgcctggga agatggtcgt g

41

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

E1
<400> 14
aagtgcactt gcaattcttt tac

23

<210> 15
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

<400> 15
tcgacgcggc cgcg

14

<210> 16
<211> 446
<212> PRT
<213> Homo sapiens

<400> 16
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
1 5 10 15
Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
20 25 30

Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
 35 40 45
 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
 50 55 60
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
 65 70 75 80
 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
 85 90 95
 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
 100 105 110
 Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
 115 120 125
 Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
 130 135 140
 Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
 145 150 155 160
 Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
 165 170 175
 Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
 180 185 190
 Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
 195 200 205
 Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 17

Asp Lys Thr His Thr Cys

1

5

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

SL
<400> 18

Met Pro Gly Lys Met Val Val

1

5